

Claims

1. Method for increasing plant yield relative to corresponding wild type plants, comprising modifying expression in a plant of a nucleic acid sequence encoding a 2xC2H2 zinc finger protein and/or modifying in a plant level and/or activity of a 2xC2H2 zinc finger protein.
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2. Method for increasing leaf surface area relative to corresponding wild type plants, comprising modifying expression in a plant of a nucleic acid sequence encoding a 2xC2H2 zinc finger protein and/or modifying in a plant level and/or activity of a 2xC2H2 zinc finger protein.
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3. Method for prolonging vegetative growth phase of a plant relative to corresponding wild type plants, comprising modifying expression in a plant of a nucleic acid sequence encoding a 2xC2H2 zinc finger protein and/or modifying in a plant level and/or activity of a 2xC2H2 zinc finger protein.
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4. Method according to any of claims 1 to 3, wherein said modifying expression, level and/or activity is effected by recombinant means and/or chemical means.
- 20 5. Method according to any of claims 1 to 4, wherein said 2xC2H2 zinc finger protein comprises a QALGGH motif.
6. Method according to any of claims 1 to 4, wherein said 2xC2H2 zinc finger protein comprises a NNM(W)QMH motif.
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7. Method according to any of claims 1 to 6, wherein said 2xC2H2 zinc finger protein comprises an EAR motif.
8. Method according to any of claims 1 to 7, wherein said 2xC2H2 zinc finger protein further comprises a B-box.
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9. Method according to any of claims 1 to 8, wherein said 2xC2H2 zinc finger protein further comprises an L-box.
- 35 10. Method according to any of claims 1 to 9, wherein said 2xC2H2 zinc finger protein is derived from a dicotyledonous plant, preferably from the family *Brassicaceae*, further preferably from *Arabidopsis thaliana*, more preferably the nucleic acid is as represented by

SEQ ID NO 2 or a homologue, derivative or active fragment thereof and/or wherein said nucleic acid is as represented by SEQ ID NO 1 or a portion thereof or sequences capable of hybridising therewith .

- 5 11. Method according to claim 10, wherein said homologue, derivative or active fragment has, in increasing order of preference, at least 30%, 31%, 32%, 33%, 34%, 35%, 36%, 37%, 38%, 39%, 40%, 41%, 42%, 43%, 44%, 45%, 46%, 47%, 48%, 49%, 50%, 52%, 54%, 56%, 58%, 60%, 62%, 64%, 66%, 68%, 70%, 72%, 74%, 76%, 78%, 80%, 82%, 84%, 86%, 88%, 90%, 92%, 94%, 96%, 98% sequence identity with the sequence of SEQ ID NO
- 10 2.
12. Method according to any of claims 1 to 11, wherein said plant is a monocot.
- 15 13. Method according to any of claims 1 to 12, wherein said modifying expression is effected by introducing into a plant a nucleic acid capable of modifying expression of a gene encoding a 2xC2H2 zinc finger protein and/or capable of modifying level and/or activity of a 2xC2H2 zinc finger protein.
- 20 14. Method according to claim 13, wherein said nucleic acid capable of modifying expression is a nucleic acid encoding a 2xC2H2 protein, such as a 2xC2H2 protein as defined in any of claims 5 to 11.
- 25 15. Method according to claims 13 or 14, wherein said nucleic acid introduced into a plant is an alternative splice variant of a nucleic acid as defined in claim 14.
- 30 16. Method according to claims 13 or 15, wherein said nucleic acid introduced into a plant is an allelic variant of a nucleic acid as defined in claim 14.
17. Method according to claims 13 or 16, wherein said nucleic acid introduced into a plant is comprised on at least part of a chromosome.
18. Method according to any of claims 1 to 17, wherein said modifying expression comprises increased expression.
- 35 19. Method according to any of claims 1 to 18, wherein expression of said nucleic acid is driven by a plant promoter, preferably a constitutive promoter, such as a GOS2 promoter.

20. Method according to any of claims 1 to 18, wherein expression of said nucleic acid is driven by a plant promoter, preferably a tissue preferred promoter, such as seed-preferred promoter.
- 5 21. Method according to any of claims 1 to 20, wherein said increased yield comprises increased above ground biomass.
22. Method according to any of claim 1 to 20, wherein said increased yield comprises increased seed yield.
- 10 23. Method according to any of claim 1 to 20, wherein said increased yield comprises increased root yield.
24. Construct comprising:
- 15 (i) A nucleic acid capable of modifying expression of a nucleic acid encoding a 2xC2H2 zinc finger protein and/or capable of modifying level and/or activity of a 2xC2H2 zinc finger protein;
- (ii) One or more plant control sequence capable of driving expression of the nucleic acid sequence of (i); and optionally
- 20 (iii) A transcription termination sequence.
25. Construct according to claim 24, wherein said nucleic acid of (i) is a nucleic acid as defined in any of claims 14 to 17.
- 25 26. Construct according to claim 24 or 25, wherein said control sequences of (ii) is at least a constitutive promoter, such as a GOS2 promoter.
27. Construct according to claim 24 or 25, wherein said control sequences of (ii) is at least a tissue preferred promoter, such as seed-preferred promoter.
- 30 28. Host cell comprising a construct according to any of claims 24 to 27.
29. Method for the production of a transgenic plant having increased yield, increased leaf surface area and/or prolonged vegetative growth, which method comprises
- 35 (i) introducing into a plant or plant cell a 2xC2H2 zinc finger nucleic acid;
- (ii) Cultivating the plant or plant cell under conditions promoting plant growth.

30. Plant obtainable by a method according to any of claims 1 to 23 and 29, which plant has increased yield, modified leaf surface area and/or prolonged vegetative growth, relative to corresponding wild type plants.
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31. Transgenic plant having increased yield, increased leaf surface area and/or prolonged vegetative growth, which transgenic plant has modified expression of a nucleic acid encoding a 2xC2H2 zinc finger protein and/or modified level and/or activity of a 2xC2H2 zinc finger protein, relative to corresponding wild type plants.
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32. Plant part, preferably a harvestable part, a propagule or progeny of a plant as defined in claim 30 or 31, which progeny has modified expression of a nucleic acid encoding 2xC2H2 zinc finger protein and/or modified level and/or activity of a 2xC2H2 zinc finger protein, relative to corresponding wild type plants.
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33. Plant or plant part according to any of claims 30 to 32, which plant is a monocotyledonous plant, preferably a cereal.
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34. Plant or plant part according to any of claims 30 to 33 selected from rice, maize, wheat, barley, millet, oats, rye, sorghum, soybean, sunflower, canola, sugarcane, alfalfa, leguminosae (bean, pea), flax, lupinus, rapeseed, tobacco, tomato, potato, squash, papaya, poplar and cotton.
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35. Use of a nucleic acid encoding a 2xC2H2 protein, of a 2xC2H2 protein and/or of a construct as defined in any of claims 24 to 27 to increase plant yield.
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36. A yield regulating composition comprising a nucleic acid encoding a 2xC2H2 protein, and/or comprising a 2xC2H2 protein, and/or comprising a construct as defined in any one of claims 24 to 27.
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37. Use of a nucleic acid encoding a 2xC2H2 protein, of a 2xC2H2 protein and/or of a construct as defined in any of claims 24 to 27 to increase leaf surface area.
38. Use of a nucleic acid encoding a 2xC2H2 protein, of a 2xC2H2 protein and/or of a construct as defined in any of claims 24 to 27 to prolong vegetative growth.

39. Use of a nucleic acid encoding a 2xC2H2 protein, of a 2xC2H2 protein and/or of a construct as defined in any of claims 24 to 27 as target for an agrochemical.
40. Use of a nucleic acid encoding a 2xC2H2 protein, of a 2xC2H2 protein and/or of a construct as defined in any of claims 24 to 27 in a breeding program.
41. Use of a plant as defined in any of claims 30 to 34 to produce enzymes, pharmaceuticals or agrochemicals.
42. Use of a plant as defined in any one of claims 30 to 34 to produce food or feed products.